

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/592,918
Source: IFWP
Date Processed by STIC: 9/25/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 09/25/2006

PATENT APPLICATION: US/10/592,918

TIME: 10:34:45

Input Set : A:\L7350.0011 SEQUENCE LISTING.txt

Output Set: N:\CRF4\09252006\J592918.raw

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3 <110> APPLICANT: Locomogene, Inc.
5 <120> TITLE OF INVENTION: Pharmaceutical composition containing hsHRD3
7 <130> FILE REFERENCE: L7350.0011
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/592,918
C--> 9 <141> CURRENT FILING DATE: 2006-09-15
9 <150> PRIOR APPLICATION NUMBER: JP 2004-76931
10 <151> PRIOR FILING DATE: 2004-03-17
12 <150> PRIOR APPLICATION NUMBER: JP 2004-314364
13 <151> PRIOR FILING DATE: 2004-10-28
15 <160> NUMBER OF SEQ ID NOS: 15
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 7885
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (46)..(2427)
29 <400> SEQUENCE: 1
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31                                     Met Arg Val Arg
32                                     1
34 ata ggg ctg acg ctg ctg ctg tgt gcg gtg ctg ctg agc ttg gcc tcg      105
35 Ile Gly Leu Thr Leu Leu Leu Cys Ala Val Leu Leu Ser Leu Ala Ser
36 5                               10                               15                               20
38 gcg tcc tcg gat gaa gaa ggc agc cag gat gaa tcc tta gat tcc aag      153
39 Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser Leu Asp Ser Lys
40                               25                               30                               35
42 act act ttg aca tca gat gag tca gta aag gac cat act act gca ggc      201
43 Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His Thr Thr Ala Gly
44                               40                               45                               50
46 aga gta gtt gct ggt caa ata ttt ctt gat tca gaa gaa tct gaa tta      249
47 Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu Glu Ser Glu Leu
48                               55                               60                               65
50 gaa tcc tct att caa gaa gag gaa gac agc ctc aag agc caa gag ggg      297
51 Glu Ser Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys Ser Gln Glu Gly
52                               70                               75                               80
54 gaa agt gtc aca gaa gat atc agc ttt cta gag tct cca aat cca gaa      345
55 Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser Pro Asn Pro Glu
56 85                               90                               95                               100
58 aac aag gac tat gaa gag cca aag aaa gta cgg aaa cca gct ttg acc      393
59 Asn Lys Asp Tyr Glu Glu Pro Lys Lys Val Arg Lys Pro Ala Leu Thr
60                               105                               110                               115

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62 gcc att gaa ggc aca gca cat ggg gag ccc tgc cac ttc cct ttt ctt      441
63 Ala Ile Glu Gly Thr Ala His Gly Glu Pro Cys His Phe Pro Phe Leu
64          120          125          130
66 ttc cta gat aag gag tat gat gaa tgt aca tca gat ggg agg gaa gat      489
67 Phe Leu Asp Lys Glu Tyr Asp Glu Cys Thr Ser Asp Gly Arg Glu Asp
68          135          140          145
70 ggc aga ctg tgg tgt gct aca acc tat gac tac aaa gca gat gaa aag      537
71 Gly Arg Leu Trp Cys Ala Thr Thr Tyr Asp Tyr Lys Ala Asp Glu Lys
72          150          155          160
74 tgg ggc ttt tgt gaa act gaa gaa gag gct gct aag aga cgg cag atg      585
75 Trp Gly Phe Cys Glu Thr Glu Glu Glu Ala Ala Lys Arg Arg Gln Met
76 165          170          175          180
78 cag gaa gca gaa atg atg tat caa act gga atg aaa atc ctt aat gga      633
79 Gln Glu Ala Glu Met Met Tyr Gln Thr Gly Met Lys Ile Leu Asn Gly
80          185          190          195
82 agc aat aag aaa agc caa aaa aga gaa gca tat cgg tat ctc caa aag      681
83 Ser Asn Lys Lys Ser Gln Lys Arg Glu Ala Tyr Arg Tyr Leu Gln Lys
84          200          205          210
86 gca gca agc atg aac cat acc aaa gcc ctg gag aga gtg tca tat gct      729
87 Ala Ala Ser Met Asn His Thr Lys Ala Leu Glu Arg Val Ser Tyr Ala
88          215          220          225
90 ctt tta ttt ggt gat tac ttg cca cag aat atc cag gca gcg aga gag      777
91 Leu Leu Phe Gly Asp Tyr Leu Pro Gln Asn Ile Gln Ala Ala Arg Glu
92          230          235          240
94 atg ttt gag aag ctg act gag gaa ggc tct ccc aag gga cag act gct      825
95 Met Phe Glu Lys Leu Thr Glu Glu Gly Ser Pro Lys Gly Gln Thr Ala
96 245          250          255          260
98 ctt ggc ttt ctg tat gcc tct gga ctt ggt gtt aat tca agt cag gca      873
99 Leu Gly Phe Leu Tyr Ala Ser Gly Leu Gly Val Asn Ser Ser Gln Ala
100          265          270          275
102 aag gct ctt gta tat tat aca ttt gga gct ctt ggg ggc aat cta ata      921
103 Lys Ala Leu Val Tyr Tyr Thr Phe Gly Ala Leu Gly Gly Asn Leu Ile
104          280          285          290
106 gcc cac atg gtt ttg ggt tac aga tac tgg gct ggc atc ggc gtc ctc      969
107 Ala His Met Val Leu Gly Tyr Arg Tyr Trp Ala Gly Ile Gly Val Leu
108          295          300          305
110 cag agt tgt gaa tct gcc ctg act cac tat cgt ctt gtt gcc aat cat      1017
111 Gln Ser Cys Glu Ser Ala Leu Thr His Tyr Arg Leu Val Ala Asn His
112          310          315          320
114 gtt gct agt gat atc tcg cta aca gga ggc tca gta gta cag aga ata      1065
115 Val Ala Ser Asp Ile Ser Leu Thr Gly Gly Ser Val Val Gln Arg Ile
116 325          330          335          340
118 cgg ctg cct gat gaa gtg gaa aat cca gga atg aac agt gga atg cta      1113
119 Arg Leu Pro Asp Glu Val Glu Asn Pro Gly Met Asn Ser Gly Met Leu
120          345          350          355
122 gaa gaa gat ttg att caa tat tac cag ttc cta gct gaa aaa ggt gat      1161
123 Glu Glu Asp Leu Ile Gln Tyr Tyr Gln Phe Leu Ala Glu Lys Gly Asp
124          360          365          370
126 gta caa gca cag gtt ggt ctt gga caa ctg cac ctg cac gga ggg cgt      1209

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127 Val Gln Ala Gln Val Gly Leu Gly Gln Leu His Leu His Gly Gly Arg
128          375          380          385
130 gga gta gaa cag aat cat cag aga gca ttt gac tac ttc aat tta gca      1257
131 Gly Val Glu Gln Asn His Gln Arg Ala Phe Asp Tyr Phe Asn Leu Ala
132          390          395          400
134 gca aat gct ggc aat tca cat gcc atg gcc ttt ttg gga aag atg tat      1305
135 Ala Asn Ala Gly Asn Ser His Ala Met Ala Phe Leu Gly Lys Met Tyr
136 405          410          415          420
138 tcg gaa gga agt gac att gta cct cag agt aat gag aca gct ctc cac      1353
139 Ser Glu Gly Ser Asp Ile Val Pro Gln Ser Asn Glu Thr Ala Leu His
140          425          430          435
142 tac ttt aag aaa gct gct gac atg ggc aac cca gtt gga cag agt ggg      1401
143 Tyr Phe Lys Lys Ala Ala Asp Met Gly Asn Pro Val Gly Gln Ser Gly
144          440          445          450
146 ctt gga atg gcc tac ctc tat ggg aga gga gtt caa gtt aat tat gat      1449
147 Leu Gly Met Ala Tyr Leu Tyr Gly Arg Gly Val Gln Val Asn Tyr Asp
148          455          460          465
150 cta gcc ctt aag tat ttc cag aaa gct gct gaa caa ggc tgg gtg gat      1497
151 Leu Ala Leu Lys Tyr Phe Gln Lys Ala Ala Glu Gln Gly Trp Val Asp
152          470          475          480
154 ggg cag cta cag ctt ggt tcc atg tac tat aat ggc att gga gtc aag      1545
155 Gly Gln Leu Gln Leu Gly Ser Met Tyr Tyr Asn Gly Ile Gly Val Lys
156 485          490          495          500
158 aga gat tat aaa cag gcc ttg aag tat ttt aat tta gct tct cag gga      1593
159 Arg Asp Tyr Lys Gln Ala Leu Lys Tyr Phe Asn Leu Ala Ser Gln Gly
160          505          510          515
162 ggc cat atc ttg gct ttc tat aac cta gct cag atg cat gcc agt ggc      1641
163 Gly His Ile Leu Ala Phe Tyr Asn Leu Ala Gln Met His Ala Ser Gly
164          520          525          530
166 acc ggc gtg atg cga tca tgt cac act gca gtg gag ttg ttt aag aat      1689
167 Thr Gly Val Met Arg Ser Cys His Thr Ala Val Glu Leu Phe Lys Asn
168          535          540          545
170 gta tgt gaa cga ggc cgt tgg tct gaa agg ctt atg act gcc tat aac      1737
171 Val Cys Glu Arg Gly Arg Trp Ser Glu Arg Leu Met Thr Ala Tyr Asn
172          550          555          560
174 agc tat aaa gat ggc gat tac aat gct gca gtg atc cag tac ctc ctc      1785
175 Ser Tyr Lys Asp Gly Asp Tyr Asn Ala Ala Val Ile Gln Tyr Leu Leu
176 565          570          575          580
178 ctg gct gaa cag ggc tat gaa gtg gca caa agc aat gca gcc ttt att      1833
179 Leu Ala Glu Gln Gly Tyr Glu Val Ala Gln Ser Asn Ala Ala Phe Ile
180          585          590          595
182 ctt gat cag aga gaa gca agc att gta ggt gag aat gaa act tat ccc      1881
183 Leu Asp Gln Arg Glu Ala Ser Ile Val Gly Glu Asn Glu Thr Tyr Pro
184          600          605          610
186 aga gct ttg cta cat tgg aac agg gcc gcc tct caa ggc tat act gtg      1929
187 Arg Ala Leu Leu His Trp Asn Arg Ala Ala Ser Gln Gly Tyr Thr Val
188          615          620          625
190 gct aga att aag ctc gga gac tac cat ttc tat ggg ttt ggc acc gat      1977
191 Ala Arg Ile Lys Leu Gly Asp Tyr His Phe Tyr Gly Phe Gly Thr Asp

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192      630      635      640
194 gta gat tat gaa act gca ttt att cat tac cgt ctg gct tct gag cag      2025
195 Val Asp Tyr Glu Thr Ala Phe Ile His Tyr Arg Leu Ala Ser Glu Gln
196 645      650      655      660
198 caa cac agt gca caa gct atg ttt aat ctg gga tat atg cat gag aaa      2073
199 Gln His Ser Ala Gln Ala Met Phe Asn Leu Gly Tyr Met His Glu Lys
200      665      670      675
202 gga ctg ggc att aaa cag gat att cac ctt gcg aaa cgt ttt tat gac      2121
203 Gly Leu Gly Ile Lys Gln Asp Ile His Leu Ala Lys Arg Phe Tyr Asp
204      680      685      690
206 atg gca gct gaa gcc agc cca gat gca caa gtt cca gtc ttc cta gcc      2169
207 Met Ala Ala Glu Ala Ser Pro Asp Ala Gln Val Pro Val Phe Leu Ala
208      695      700      705
210 ctc tgc aaa ttg ggc gtc gtc tat ttc ttg cag tac ata cgg gaa aca      2217
211 Leu Cys Lys Leu Gly Val Val Tyr Phe Leu Gln Tyr Ile Arg Glu Thr
212      710      715      720
214 aac att cga gat atg ttc acc caa ctt gat atg gac cag ctt ttg gga      2265
215 Asn Ile Arg Asp Met Phe Thr Gln Leu Asp Met Asp Gln Leu Leu Gly
216 725      730      735      740
218 cct gag tgg gac ctt tac ctc atg acc atc att gcg ctg ctg ttg gga      2313
219 Pro Glu Trp Asp Leu Tyr Leu Met Thr Ile Ala Leu Leu Leu Gly
220      745      750      755
222 aca gtc ata gct tac agg caa agg cag cac caa gac atg cct gca ccc      2361
223 Thr Val Ile Ala Tyr Arg Gln Arg Gln His Gln Asp Met Pro Ala Pro
224      760      765      770
226 agg cct cca ggg cca cgg cca gct cca ccc cag cag gag ggg cca cca      2409
227 Arg Pro Pro Gly Pro Arg Pro Ala Pro Pro Gln Gln Glu Gly Pro Pro
228      775      780      785
230 gag cag cag cca cca cag taataggcac tgggtccagc cttgatcagt      2457
231 Glu Gln Gln Pro Pro Gln
232      790
234 gacagcgaag gaagttatct gctgggaaca cttgcatttg atttaggacc ttggatcagt      2517
236 ggtcacctcc cagaagaggc acggcacaag gaagcattga attcctaaag ctgcttagaa      2577
238 tctgatgcct ttattttcag ggataagtaa ctcttaccta aactgagctg aatgtttgtt      2637
240 tcagtgccat atggagtaac aactttcagt ggcttttttt tttcttttct ggaaacatat      2697
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244 attatttcag tgtgcataag ttcttaattgt caaccatctt taagggtattg tgcacgcaca      2817
246 ctaaaaaactg atcagtgtta aaaaggaaaa ccagtttgca agtttaaacg tgttcgaaag      2877
248 tctgaaaata gaacttgctt ttttaagttaa aaaaaaaaaa aaagctatct tgaaaatggt      2937
250 ttggaactgc gataactgag aaactttctta ccagtccaca tgcaattaaa catattcagc      2997
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254 taccatactc ctctccttca aagaatgaaa ggccttggtta aggagttttt tgtgagcttt      3117
256 acttcttttg aatggaatat acttatgcaa aaccttggtga actgactcct tgcactaacg      3177
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260 tccagaagcc agaggatgga ctaagtggga gaaattagaa aacaaaacga actctggttg      3297
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264 atttatttta ctttgcattt ctttttgcac aaagaacaca tcaccttcct gaattcttta      3417
266 aatatgaaat atcattgcca gggtatggct tacagtgact actattatca atactaaaac      3477
268 tcagagaatc aaagatggat taaactcagt ggttgatgaa agccaaaacc tgtttgtact      3537

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270 gttctatact attcaggtat ctttttattt ctgatagttt tatattataa tagaaagcca 3597
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274 tactatgctt caggattgtc tgggttaaata gtatgggaaa aaaactgaag agtttcaaca 3717
276 taattacaca cgtgaaataa ttacagctta aactgaattt gtatttcatt ttattgtcag 3777
278 atgggtggtgt tcaccagcct gtatcttgtc tgagactgca ttcgtatctg agcagggtttt 3837
280 ctatgcctac tgatgtcagt atgtttatac taaccttcac gcttttttcc cagaatccct 3897
282 catctgccag aaaacttgaa aggtttattg cttgtagagt tgtactgctt tgatttttga 3957
284 agttggggta gtagttagaa cttagatttaa ctagtctata atgaacatga aggcctttat 4017
286 atatgaagtt gtataccttt ttgtgtttag agaattatgg gaaacctggg aagcaaaact 4077
288 ttcctcccag ataattgctt ccaaattcga agagttagtc accaagagag ccatatgtat 4137
290 gaaagcgtat ctgtgaaagg taggaaactt acccccctta agtgtaatgt tgcttttaggc 4197
292 aactcttgta aatagtgaga cttgtttggt ctcttacatg tagagatttg agtgcagttg 4257
294 gtacagtact ttggtgtctc caccactgtc ccttctcccc gcttcaaaat aagtgtaatc 4317
296 cacggtagca gccacacttc cttcagaagg aactgttata atttatttaa aagttgaaaa 4377
298 accacccaag atgactacca actttcactt tttttcttct gccatccacc ctcattttcc 4437
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302 acattttctta aaacagtgtg tgccacctaa ggctggatgg gaaagtgcag tcttgttggt 4557
304 catataaaaa acacacttct tattagttta cccacttgcc tttttctatt gttaatgttc 4617
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362 ggaagtttta aatagacctt aagctggcat tgtgaaggaa caccatggta gactcttttt 6357
364 ggtaatggta ttttgtattt aatgaaatgc agtataaagg ttggtgaagt gtaataataa 6417
366 ttgtgtaaac aaatcctggt taatagaaga gatgtacaga atcgttttgg tactgtatct 6477

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/25/2006
PATENT APPLICATION: US/10/592,918 TIME: 10:34:46

Input Set : A:\L7350.0011 SEQUENCE LISTING.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,8,9,10,11,12,13,14,15

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/592,918

DATE: 09/25/2006

TIME: 10:34:46

Input Set : A:\L7350.0011 SEQUENCE LISTING.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date